

1636

RAW SEQUENCE LISTING DATE: 02/06/2001
 PATENT APPLICATION: US/09/242,657B TIME: 14:59:27

Input Set : A:\Sequence Listing (55411.2).txt
 Output Set: N:\CRF3\02062001\I242657B.raw

**Does Not Comply
 Corrected Diskette Needed**

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 4 (i) APPLICANT: Peter Ruhdal Jensen
 5 Karin Hammer
 7 (ii) TITLE OF INVENTION: Artificial promoter libraries
 8 for selected organisms and promoters derived from such
 9 libraries
 11 (iii) NUMBER OF SEQUENCES: 58
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Stanislaus Aksman
 15 Hunton & Williams
 16 (B) STREET: 1900 K Street, NW
 17 (C) CITY: Washington, DC
 18 (E) COUNTRY: USA
 19 (F) ZIP: 20006-1109
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 26 (EPO)
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/242,657B
 C--> 30 (B) FILING DATE: 19-Feb-1999
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: DK 886/96
 34 (B) FILING DATE: 23-AUG-1996
 35 (A) APPLICATION NUMBER: PCT/DK97/00342
 36 (B) FILING DATE: August 25, 1997
 38 (viii) ATTORNEY/AGENT INFORMATION:
 C--> 39 (C) REFERENCE/DOCKET NUMBER: 55411.000002
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: (202) 955-1500
 43 (B) TELEFAX: (202) 778-2201

ERRORED SEQUENCES

45 (2) INFORMATION FOR SEQ ID NO: 1:
 47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 100 base pairs
 49 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 51 (D) TOPOLOGY: linear
 53 (ii) MOLECULE TYPE: DNA (genomic)
 55 (iii) HYPOTHETICAL: YES
 56 (iv) ANTI-SENSE: NO

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FEB 14 2001

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58      (vi) ORIGINAL SOURCE:
59          (A) ORGANISM: Lactococcus lactis
61      (ix) FEATURE:
62          (A) NAME/KEY: promoter
63          (B) LOCATION:26..82
64          (C) IDENTIFICATION METHOD: experimental
65          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
66 /standard_name= "Artificial promoter library" /note= "A
67 degenerated sequence specifying a mixture of artificial
68 promoters covering a wide range of expression in small steps
69 in L. lactis"
71      (ix) FEATURE:
72          (A) NAME/KEY: misc_feature
73          (B) LOCATION:31..45
74          (D) OTHER INFORMATION:/standard_name= "Consensus
75 sequence"
77      (ix) FEATURE:
78          (A) NAME/KEY: misc_feature
79          (B) LOCATION:60..69
80          (D) OTHER INFORMATION:/standard_name= "Consensus
81 sequence"
83      (ix) FEATURE:
84          (A) NAME/KEY: misc_feature
85          (B) LOCATION:74..82
86          (D) OTHER INFORMATION:/standard_name= "Consensus
87 sequence"
89      (ix) FEATURE:
90          (A) NAME/KEY: -35_signal
91          (B) LOCATION:40..45
92          (D) OTHER INFORMATION:/standard_name= "-35 box"
94      (ix) FEATURE:
95          (A) NAME/KEY: -10_signal
96          (B) LOCATION:63..68
97          (D) OTHER INFORMATION:/standard_name= "Pribnow box"
99      (ix) FEATURE:
100          (A) NAME/KEY: misc_recomb
101          (B) LOCATION:3..25
102          (C) IDENTIFICATION METHOD: experimental
103          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
104 /standard_name= "Multiple cloning site" /label= MCS
105 /note= "A sequence specifying recognition sites
106 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
107 MboI,
108 DpnI, AflII, MseI, SspI, NsiI."
110      (ix) FEATURE:
111          (A) NAME/KEY: misc_recomb
112          (B) LOCATION:74..98
113          (C) IDENTIFICATION METHOD: experimental
114          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL

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115 /standard_name= "Multiple cloning site"
116 /label= MCS
117 /note= "A sequence specifying recognition sites
118 for the restriction endonucleases: ScaI, RsaI, HpaI, HincII,
119 MseI, SfcI,
120 PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, EcoRI."
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 124 CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN
125 NNNNNNNNNNT 60.
127 GGTATAATAN NANAGTACTG TTAAGTGCAG CTGAATTCGG          100
129 (2) INFORMATION FOR SEQ ID NO: 2:
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 113 base pairs
133 (B) TYPE: nucleic acid
134 (C) STRANDEDNESS: double
135 (D) TOPOLOGY: linear
137 (ii) MOLECULE TYPE: DNA (genomic)
139 (iii) HYPOTHETICAL: YES
141 (iv) ANTI-SENSE: NO
143 (ix) FEATURE:
144 (A) NAME/KEY: promoter
145 (B) LOCATION:23..95
146 (D) OTHER INFORMATION:/standard_name=
147 "Artificial promoter library"
148 /note= "A degenerated sequence specifying a mixture
149 of artificial temperature regulated promoters covering a wide
150 range of expression in small steps in L. lactis"
152 (ix) FEATURE:
153 (A) NAME/KEY: misc_feature
154 (B) LOCATION:23..49
155 (D) OTHER INFORMATION:/standard_name=
156 "Sequence providing temperature regulation to promoters"
157 /note= "This sequence comprising two inverted
158 repeats separated by a short spacer provides temperature (heat
159 shock) regulation to promoters in Gram-positive bacteria"
161 (ix) FEATURE:
162 (A) NAME/KEY: misc_feature
163 (B) LOCATION:50..60
164 (D) OTHER INFORMATION:/standard_name=
165 "Consensus sequence"
167 (ix) FEATURE:
168 (A) NAME/KEY: misc_feature
169 (B) LOCATION:75..84
170 (D) OTHER INFORMATION:/standard_name= "Consensus
171 sequence"
173 (ix) FEATURE:
174 (A) NAME/KEY: misc_feature
175 (B) LOCATION:89..95
176 (D) OTHER INFORMATION:/standard_name= "Consensus

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60 format error

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177 sequence"
179     (ix) FEATURE:
180         (A) NAME/KEY: -35_signal
181         (B) LOCATION:55..60
182         (D) OTHER INFORMATION:/standard_name= "-35 box"
184     (ix) FEATURE:
185         (A) NAME/KEY: -10_signal
186         (B) LOCATION:78..83
187         (D) OTHER INFORMATION:/standard_name= "Pribnow box"
189     (ix) FEATURE:
190         (A) NAME/KEY: misc_recomb
191         (B) LOCATION:3..22
192         (D) OTHER INFORMATION:/standard_name= "Multiple
193 cloning site"
194 /label= MCS
195 /note= "A sequence specifying recognition sites
196 for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI,
197 MboI,DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."
199     (ix) FEATURE:
200         (A) NAME/KEY: misc_recomb
201         (B) LOCATION:89..111
202         (D) OTHER INFORMATION:/standard_name= "Multiple
203 cloning site"
204 /label= MCS
205 /note= "A sequence specifying recognition sites
206 for the restriction endonucleases: ScaI, RsaI, SfcI, PstI,
207 Fnu4HI, BbvI,
208 PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."
210     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 212 CGGGATCCAA GCTTAATATT AATTAGCACT· CNNNNNNNNN GAGTGCTAAT →60
213 TTTTGTGACA 60
E--> 215 NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG →113
W--> 216 113
218 (2) INFORMATION FOR SEQ ID NO: 3:
220     (i) SEQUENCE CHARACTERISTICS:
221         (A) LENGTH: 199 base pairs
222         (B) TYPE: nucleic acid
223         (C) STRANDEDNESS: double
224         (D) TOPOLOGY: linear
226     (ii) MOLECULE TYPE: DNA (genomic)
228     (iii) HYPOTHETICAL: YES
230     (iv) ANTI-SENSE: NO
232     (vi) ORIGINAL SOURCE:
233         (A) ORGANISM: Saccharomyces cerevisiae
235     (ix) FEATURE:
236         (A) NAME/KEY: protein_bind
237         (B) LOCATION:10..16
238         (D) OTHER INFORMATION:/function= "Activating
239 promoters in

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240 S. cerevisiae"
241 /bound_moiety= "GCN4 protein"
242 /standard_name= "Upstream activating sequence" /label=
243 UAS_GCN4p
244 /note= "A DNA sequence that specifies a binding
245 site for the GCN4 protein, which activates the transcription
246 of genes involved in amino acid synthesis in S. cerevisiae."
248 (ix) FEATURE:
249 (A) NAME/KEY: TATA_signal
250 (B) LOCATION:67..72
251 (D) OTHER INFORMATION:/standard_name= "TATA box"
253 (ix) FEATURE:
254 (A) NAME/KEY: misc_signal
255 (B) LOCATION:122..144
256 (D) OTHER INFORMATION:/function= "Transcription
257 initiation"
258 /standard_name= "TI box"
260 (ix) FEATURE:
261 (A) NAME/KEY: protein_bind
262 (B) LOCATION:122..144
263 (D) OTHER INFORMATION:/bound_moiety= "Arginine
264 repressor"
265 /standard_name= "arginine repressor binding
266 site"
267 /label= argR
269 (ix) FEATURE:
270 (A) NAME/KEY: misc_RNA
271 (B) LOCATION:145..192
272 (D) OTHER INFORMATION:/function= "Spacer"
273 /standard_name= "Part of native sequence for
274 ARG8
275 gene incl. first codon"
277 (ix) FEATURE:
278 (A) NAME/KEY: misc_recomb
279 (B) LOCATION:3..8
280 (D) OTHER INFORMATION:/standard_name= "Recognition
281 site for restriction endonuclease EcoRI"
282 /label= EcoRI_site
284 (ix) FEATURE:
285 (A) NAME/KEY: misc_recomb
286 (B) LOCATION:192..197
287 (D) OTHER INFORMATION:/standard_name= "Recognition
288 site or restriction endonuclease BamHI"
289 /label= BamHI_site
291 (ix) FEATURE:
292 (A) NAME/KEY: promoter
293 (B) LOCATION:10..192
294 (D) OTHER INFORMATION:/standard_name= "Artificial
295 promoter library"

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296 /note= "A degenerated sequence specifying a mixture
297 of
298 artificial promoters covering a wide range of
299 expression in small steps in S. cerevisiae"
301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 303 CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
304 NNNNNNNNNN 60
E--> 306 NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN
307 NNNNNNNNNN 120
E--> 309 NCTCTTAAGT GCAAGTGA CTGCAACATTT TTTTCGTTT TTAGAATAAT
310 TCAAGAATCG 180
E--> 312 CTACCAATCA TGGATCCCG
W--> 313 199
346 (2) INFORMATION FOR SEQ ID NO: 5:
348 (i) SEQUENCE CHARACTERISTICS:
349 (A) LENGTH: 60 base pairs
350 (B) TYPE: nucleic acid
351 (C) STRANDEDNESS: double
352 (D) TOPOLOGY: linear
354 (ii) MOLECULE TYPE: DNA (genomic)
356 (iii) HYPOTHETICAL: YES
358 (iv) ANTI-SENSE: NO
360 (vi) ORIGINAL SOURCE:
361 (A) ORGANISM: Lactococcus lactis
363 (ix) FEATURE:
364 (A) NAME/KEY: promoter
365 (B) LOCATION:4..60
366 (D) OTHER INFORMATION:/standard_name=
367 "Constitutional promoter"
368 /label= Cpl
370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 372 CATACCGGAG TTTATTCTTG ACAGTTCAC CTCGGGTTGA TATAATATCT
373 CAGTACTGTT 60
375 (2) INFORMATION FOR SEQ ID NO: 6:
377 (i) SEQUENCE CHARACTERISTICS:
378 (A) LENGTH: 60 base pairs
379 (B) TYPE: nucleic acid
380 (C) STRANDEDNESS: double
381 (D) TOPOLOGY: linear
383 (ii) MOLECULE TYPE: DNA (genomic)
385 (iii) HYPOTHETICAL: YES
386 (iv) ANTI-SENSE: NO
388 (vi) ORIGINAL SOURCE:
389 (A) ORGANISM: Lactococcus lactis
391 (ix) FEATURE:
392 (A) NAME/KEY: promoter
393 (B) LOCATION:4..60
394 (D) OTHER INFORMATION:/standard_name=
395 "Constitutional promoter"

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396 /label= Cp10
398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 400 CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA
401 CAGTACTGTT 60
403 (2) INFORMATION FOR SEQ ID NO: 7:
405 (i) SEQUENCE CHARACTERISTICS:
406 (A) LENGTH: 59 base pairs
407 (B) TYPE: nucleic acid
408 (C) STRANDEDNESS: double
409 (D) TOPOLOGY: linear
411 (ii) MOLECULE TYPE: DNA (genomic)
413 (iii) HYPOTHETICAL: YES
415 (iv) ANTI-SENSE: NO
417 (vi) ORIGINAL SOURCE:
418 (A) ORGANISM: Lactococcus lactis
420 (ix) FEATURE:
421 (A) NAME/KEY: promoter
422 (B) LOCATION:4..59
423 (D) OTHER INFORMATION:/standard_name=
424 "Constitutional promoter"
425 /label= Cp11
426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 428 CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCTTTGA TATAATAAGT
429 AGTACTGTT 59
431 (2) INFORMATION FOR SEQ ID NO: 8:
433 (i) SEQUENCE CHARACTERISTICS:
434 (A) LENGTH: 60 base pairs
435 (B) TYPE: nucleic acid
436 (C) STRANDEDNESS: double
437 (D) TOPOLOGY: linear
439 (ii) MOLECULE TYPE: DNA (genomic)
441 (iii) HYPOTHETICAL: YES
443 (iv) ANTI-SENSE: NO
445 (vi) ORIGINAL SOURCE:
446 (A) ORGANISM: Lactococcus lactis
447 (ix) FEATURE:
448 (A) NAME/KEY: promoter
449 (B) LOCATION:4..60
450 (D) OTHER INFORMATION:/standard_name=
451 "Constitutional promoter"
452 /label= Cp12
454 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 456 CATATACAAG TTTATTCTTG AACTAGTCG GCCAAAATGA TATAATACCT
457 GAGTACTGTT 60
459 (2) INFORMATION FOR SEQ ID NO: 9:
461 (i) SEQUENCE CHARACTERISTICS:
462 (A) LENGTH: 60 base pairs
463 (B) TYPE: nucleic acid
464 (C) STRANDEDNESS: double

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465         (D) TOPOLOGY: linear
467     (ii) MOLECULE TYPE: DNA (genomic)
469     (iii) HYPOTHETICAL: YES
471     (iv) ANTI-SENSE: NO
473     (vi) ORIGINAL SOURCE:
474         (A) ORGANISM: Lactococcus lactis
476     (ix) FEATURE:
477         (A) NAME/KEY: promoter
478         (B) LOCATION:4..60
479         (D) OTHER INFORMATION:/standard_name=
480 "Constitutional promoter"
481 /label= Cp13
483     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 485 CATGCTTTAC TTTATTCTTG ACAAACCAC CAGCTTTTGG TATAATACGT
486 GAGAACTGTT 60
488 (2) INFORMATION FOR SEQ ID NO: 10:
490     (i) SEQUENCE CHARACTERISTICS:
491         (A) LENGTH: 60 base pairs
492         (B) TYPE: nucleic acid
493         (C) STRANDEDNESS: double
494         (D) TOPOLOGY: linear
496     (ii) MOLECULE TYPE: DNA (genomic)
498     (iii) HYPOTHETICAL: YES
500     (iv) ANTI-SENSE: NO
502     (vi) ORIGINAL SOURCE:
503         (A) ORGANISM: Lactococcus lactis
505     (ix) FEATURE:
506         (A) NAME/KEY: promoter
507         (B) LOCATION:4..60
508         (D) OTHER INFORMATION:/standard_name=
509 "Constitutional promoter"
510 /label= Cp14
512     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 514 CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA
515 CAGTACTGTT 60
517 (2) INFORMATION FOR SEQ ID NO: 11:
519     (i) SEQUENCE CHARACTERISTICS:
520         (A) LENGTH: 60 base pairs
521         (B) TYPE: nucleic acid
522         (C) STRANDEDNESS: double
523         (D) TOPOLOGY: linear
525     (ii) MOLECULE TYPE: DNA (genomic)
527     (iii) HYPOTHETICAL: YES
529     (iv) ANTI-SENSE: NO
531     (vi) ORIGINAL SOURCE:
532         (A) ORGANISM: Lactococcus lactis
534     (ix) FEATURE:
535         (A) NAME/KEY: promoter
536         (B) LOCATION:4..60

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